```
        FILE 'MEDLINE, BIOSIS, EMBASE, SCISEARCH, CAPLUS, USPATFULL, PCTFULL'
        ENTERED AT 12:13:03 ON 12 JAN 2006
L1          42112 S TRANSMEMBRANE (W) (PROTEIN? OR POLYPEPTIDE?)
L2             83 S CYSTATIN(W)LIKE(W)DOMAIN
L3              1 S L1 AND L2
L4           1286 S (ALPHA OR A)(W)2(W)HS(W)GLYCOPROTEIN
L5              1 S L1 AND L2 AND L3
L6              1 S L1 AND L3
L7              1 S L2 AND L3
L8        3205318 S (INFLAMMAT? OR (CANCER OR TUMOR) OR PROLIFERAT? OR DIFFERENTI
L9            162 S L4(P)L8
L10           258 S L4(S)L8
L11            94 DUP REM L9 (68 DUPLICATES REMOVED)
L12            29 S 1950-1998/PY AND L11

=>
```

# Refine Search

### Search Results -

| Terms | Documents |
|---|---|
| L1 and L2 and L3 | 1 |

**Database:**

US Pre-Grant Publication Full-Text Database
US Patents Full-Text Database
US OCR Full-Text Database
EPO Abstracts Database
JPO Abstracts Database
Derwent World Patents Index
IBM Technical Disclosure Bulletins

**Search:**

[ Refine Search ]

[ Recall Text ⬍ ]    [ Clear ]    [ Interrupt ]

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### Search History

---

**DATE:  Thursday, January 12, 2006**    Printable Copy    Create Case

| Set Name | Query | Hit Count | Set Name |
|---|---|---|---|
| side by side | | | result set |
| | *DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=YES; OP=OR* | | |
| L5 | L1 and L2 and L3 | 1 | L5 |
| L4 | L1 same L2 same L3 | 0 | L4 |
| L3 | (alpha or a) adj 2 adj glycoprotein | 97 | L3 |
| L2 | cystatin NEAR1 domain | 32 | L2 |
| L1 | transmembrane adj (protein$1 or polypeptide$1) | 9646 | L1 |

END OF SEARCH HISTORY

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OM protein - protein search, using sw model

Run on:          December 16, 2005, 19:14:03 ; Search time 190 Seconds
                                             (without alignments)
                                             883.383 Million cell updates/sec

Title:           US-10-626-686-1
Perfect score:   2018
Sequence:        1 MGLLLPLALCILVLCCGAMS..........ARTAECPGPAQNASPLVLPP 382

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters:      2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       A_Geneseq_21:*
                 1:  geneseqp1980s:*
                 2:  geneseqp1990s:*
                 3:  geneseqp2000s:*
                 4:  geneseqp2001s:*
                 5:  geneseqp2002s:*
                 6:  geneseqp2003as:*
                 7:  geneseqp2003bs:*
                 8:  geneseqp2004s:*
                 9:  geneseqp2005s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                   SUMMARIES
                     %
Result            Query
   No.    Score   Match  Length DB   ID                        Description
------------------------------------------------------------------------------
       1    2018  100.0     382  2   AAW88491                  Aaw88491 Human liv
       2    2018  100.0     382  3   AAB25782                  Aab25782 Human sec
       3    2018  100.0     382  4   AAB75368                  Aab75368 Human sec
       4    2018  100.0     382  8   ADP19169                  Adp19169 Human sec
       5    2015   99.9     382  4   AAB51346                  Aab51346 Human HS-
       6    2010   99.6     382  8   ADJ75395                  Adj75395 Marker ge
       7    2001   99.2     382  7   ADE40170                  Ade40170 Human NOV
       8  1925.5   95.4     369  7   ADE40172                  Ade40172 Human NOV

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OM protein - protein search, using sw model

Run on:          December 16, 2005, 19:18:29 ; Search time 48 Seconds
                                              (without alignments)
                                              657.961 Million cell updates/sec

Title:          US-10-626-686-1
Perfect score:  2018
Sequence:       1 MGLLLPLALCILVLCCGAMS.........ARTAECPGPAQNASPLVLPP 382

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters:      572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      Issued_Patents_AA:*
                1:  /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
                2:  /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
                3:  /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
                4:  /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                5:  /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                6:  /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES

|        |       | %     |        |    |                    |                 |
| Result |       | Query |        |    |                    |                 |
| No.    | Score | Match | Length | DB | ID                 | Description     |
|--------|-------|-------|--------|----|--------------------|-----------------|
| 1      | 2018  | 100.0 | 382    | 2  | US-09-599-360B-93  | Sequence 93, Appl  |
| 2      | 1632  | 80.9  | 314    | 2  | US-09-949-016-11341 | Sequence 11341, A |
| 3      | 421   | 20.9  | 81     | 2  | US-09-513-999C-7797 | Sequence 7797, Ap |
| 4      | 274   | 13.6  | 367    | 1  | US-08-737-045-14   | Sequence 14, Appl  |
| 5      | 274   | 13.6  | 367    | 2  | US-08-932-871B-2   | Sequence 2, Appli  |
| 6      | 274   | 13.6  | 367    | 2  | US-09-476-919-2    | Sequence 2, Appli  |
| 7      | 274   | 13.6  | 367    | 2  | US-08-780-311A-2   | Sequence 2, Appli  |
| 8      | 265.5 | 13.2  | 364    | 1  | US-08-483-926A-10  | Sequence 10, Appl  |
| 9      | 265.5 | 13.2  | 364    | 1  | US-08-737-045-10   | Sequence 10, Appl  |
| 10     | 254   | 12.6  | 349    | 1  | US-08-483-926A-12  | Sequence 12, Appl  |
| 11     | 253.5 | 12.6  | 361    | 1  | US-08-483-926A-9   | Sequence 9, Appli  |

OM protein - protein search, using sw model

Run on:          December 16, 2005, 19:26:49 ; Search time 163 Seconds
                                              (without alignments)
                                              979.207 Million cell updates/sec

Title:           US-10-626-686-1
Perfect score:   2018
Sequence:        1 MGLLLPLALCILVLCCGAMS..........ARTAECPGPAQNASPLVLPP 382

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters:      1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Published_Applications_AA_Main:*
                 1:  /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
                 2:  /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
                 3:  /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
                 4:  /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
                 5:  /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
                 6:  /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 2018 | 100.0 | 382 | 3 | US-09-978-360A-425 | Sequence 425, App |
| 2 | 2018 | 100.0 | 382 | 4 | US-10-315-664-93 | Sequence 93, Appl |
| 3 | 2018 | 100.0 | 382 | 5 | US-10-626-686-1 | Sequence 1, Appli |
| 4 | 2010 | 99.6 | 382 | 5 | US-10-631-467-647 | Sequence 647, App |
| 5 | 2001 | 99.2 | 382 | 4 | US-10-210-172-76 | Sequence 76, Appl |
| 6 | 1925.5 | 95.4 | 369 | 4 | US-10-210-172-78 | Sequence 78, Appl |
| 7 | 1925.5 | 95.4 | 369 | 4 | US-10-210-172-80 | Sequence 80, Appl |
| 8 | 1833 | 90.8 | 356 | 4 | US-10-210-172-84 | Sequence 84, Appl |
| 9 | 1787.5 | 88.6 | 345 | 4 | US-10-210-172-86 | Sequence 86, Appl |
| 10 | 1612.5 | 79.9 | 317 | 4 | US-10-210-172-82 | Sequence 82, Appl |
| 11 | 274 | 13.6 | 367 | 5 | US-10-626-686-57 | Sequence 57, Appl |

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OM protein - protein search, using sw model

Run on:           December 16, 2005, 19:26:00 ; Search time 12 Seconds
                                             (without alignments)
                                  214.454 Million cell updates/sec

Title:            US-10-626-686-1
Perfect score:    2018
Sequence:         1 MGLLLPLALCILVLCCGAMS..........ARTAECPGPAQNASPLVLPP 382

Scoring table:    BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched:         51470 seqs, 6736768 residues

Total number of hits satisfying chosen parameters:      51470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        Published_Applications_AA_New:*
                  1:  /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
                  2:  /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
                  3:  /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
                  4:  /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
                  5:  /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
                  6:  /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
                  7:  /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
                  8:  /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                               SUMMARIES
                     %
Result            Query
   No.    Score   Match  Length  DB   ID                        Description
   ------------------------------------------------------------------------------
        1    274   13.6     367   6   US-10-888-962-6           Sequence 6, Appli
        2  245.5   12.2     352   6   US-10-888-962-8           Sequence 8, Appli
        3    242   12.0     345   6   US-10-888-962-7           Sequence 7, Appli
        4    242   12.0     359   6   US-10-888-962-5           Sequence 5, Appli
        5    110    5.5    1005   7   US-11-113-424-63          Sequence 63, Appl
        6     99    4.9     448   6   US-10-967-527A-16         Sequence 16, Appl
        7   96.5    4.8    1142   7   US-11-044-051-73          Sequence 73, Appl
        8     95    4.7     437   6   US-10-995-561-931         Sequence 931, App
        9     95    4.7     447   6   US-10-995-561-930         Sequence 930, App
```

```
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OM protein - protein search, using sw model

Run on:          December 16, 2005, 19:18:49 ; Search time 573 Seconds
                                             (without alignments)
                                             921.303 Million cell updates/sec

Title:           US-10-626-686-1
Perfect score:   2018
Sequence:        1 MGLLLPLALCILVLCCGAMS..........ARTAECPGPAQNASPLVLPP 382

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        7861189 seqs, 1381955077 residues

Total number of hits satisfying chosen parameters:      7861189

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Pending_Patents_AA_Main:*
                 1:   /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep:*
                 2:   /cgn2_6/ptodata/1/paa/US066_COMB.pep:*
                 3:   /cgn2_6/ptodata/1/paa/US073_COMB.pep:*
                 4:   /cgn2_6/ptodata/1/paa/US074_COMB.pep:*
                 5:   /cgn2_6/ptodata/1/paa/US075_COMB.pep:*
                 6:   /cgn2_6/ptodata/1/paa/US076_COMB.pep:*
                 7:   /cgn2_6/ptodata/1/paa/US077_COMB.pep:*
                 8:   /cgn2_6/ptodata/1/paa/US078_COMB.pep:*
                 9:   /cgn2_6/ptodata/1/paa/US079_COMB.pep:*
                 10:  /cgn2_6/ptodata/1/paa/US080_COMB.pep:*
                 11:  /cgn2_6/ptodata/1/paa/US081_COMB.pep:*
                 12:  /cgn2_6/ptodata/1/paa/US082_COMB.pep:*
                 13:  /cgn2_6/ptodata/1/paa/US083_COMB.pep:*
                 14:  /cgn2_6/ptodata/1/paa/US084_COMB.pep:*
                 15:  /cgn2_6/ptodata/1/paa/US085_COMB.pep:*
                 16:  /cgn2_6/ptodata/1/paa/US086_COMB.pep:*
                 17:  /cgn2_6/ptodata/1/paa/US087_COMB.pep:*
                 18:  /cgn2_6/ptodata/1/paa/US088_COMB.pep:*
                 19:  /cgn2_6/ptodata/1/paa/US089_COMB.pep:*
                 20:  /cgn2_6/ptodata/1/paa/US090_COMB.pep:*
                 21:  /cgn2_6/ptodata/1/paa/US091_COMB.pep:*
                 22:  /cgn2_6/ptodata/1/paa/US092_COMB.pep:*
                 23:  /cgn2_6/ptodata/1/paa/US093_COMB.pep:*
                 24:  /cgn2_6/ptodata/1/paa/US094_COMB.pep:*
                 25:  /cgn2_6/ptodata/1/paa/US095_COMB.pep:*
                 26:  /cgn2_6/ptodata/1/paa/US096_COMB.pep:*
                 27:  /cgn2_6/ptodata/1/paa/US097_COMB.pep:*
```

OM protein - protein search, using sw model

Run on:            December 16, 2005, 19:22:10 ; Search time 14 Seconds
                                              (without alignments)
                                              262.433 Million cell updates/sec

Title:            US-10-626-686-1
Perfect score:    2018
Sequence:         1 MGLLLPLALCILVLCCGAMS..........ARTAECPGPAQNASPLVLPP 382

Scoring table:    BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched:         57320 seqs, 9617956 residues

Total number of hits satisfying chosen parameters:      57320

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        Pending_Patents_AA_New:*
                  1:  /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*
                  2:  /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
                  3:  /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
                  4:  /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
                  5:  /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
                  6:  /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
                  7:  /cgn2_6/ptodata/1/paa/US11_NEW_COMB.pep:*
                  8:  /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                  %
Result            Query
   No.    Score  Match Length DB  ID                          Description
-------------------------------------------------------------------------------
        1    274   13.6    367  7  US-11-268-554-157           Sequence 157, App
        2    274   13.6    367  7  US-11-268-554-158           Sequence 158, App
        3  267.5   13.3    366  7  US-11-268-554-159           Sequence 159, App
        4  188.5    9.3    204  7  US-11-268-554-156           Sequence 156, App
        5    103    5.1   1015  1  PCT-US05-38668-14           Sequence 14, Appl
        6    103    5.1   1015  1  PCT-US05-28839A-82          Sequence 82, Appl
        7    103    5.1   1015  7  US-11-259-133-14            Sequence 14, Appl
        8    103    5.1   1015  7  US-11-203-251A-82           Sequence 82, Appl
        9    103    5.1   1037  1  PCT-US05-38668-12           Sequence 12, Appl

OM protein - protein search, using sw model

Run on:          December 16, 2005, 19:15:33 ; Search time 39 Seconds
                                             (without alignments)
                                             942.431 Million cell updates/sec

Title:           US-10-626-686-1
Perfect score:   2018
Sequence:        1 MGLLLPLALCILVLCCGAMS..........ARTAECPGPAQNASPLVLPP 382

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:      283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       PIR_80:*
                 1:  pir1:*
                 2:  pir2:*
                 3:  pir3:*
                 4:  pir4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 274 | 13.6 | 367 | 1 | WOHU | alpha-2-HS-glycopr |
| 2 | 265.5 | 13.2 | 364 | 2 | S22394 | fetuin precursor - |
| 3 | 257.5 | 12.8 | 362 | 2 | S22395 | fetuin precursor - |
| 4 | 245 | 12.1 | 375 | 2 | A32827 | fetuin precursor - |
| 5 | 242 | 12.0 | 345 | 2 | S21094 | alpha-2-HS-glycopr |
| 6 | 242 | 12.0 | 359 | 2 | A35714 | fetuin precursor - |
| 7 | 236.5 | 11.7 | 348 | 2 | JC5431 | countertrypin prec |
| 8 | 224 | 11.1 | 525 | 1 | KGHUGH | histidine-rich gly |
| 9 | 211 | 10.5 | 445 | 2 | A60488 | histidine-rich gly |
| 10 | 204.5 | 10.1 | 434 | 1 | KGBOL2 | kininogen, LMW II |
| 11 | 204.5 | 10.1 | 436 | 1 | KGBOL1 | kininogen, LMW I p |
| 12 | 204.5 | 10.1 | 619 | 1 | KGBOH2 | kininogen, HMW II |
| 13 | 204.5 | 10.1 | 621 | 1 | KGBOH1 | kininogen, HMW I p |

OM protein - protein search, using sw model

Run on:          December 16, 2005, 19:14:43 ; Search time 231 Seconds
                                              (without alignments)
                                 1166.718 Million cell updates/sec

Title:           US-10-626-686-1
Perfect score:   2018
Sequence:        1 MGLLLPLALCILVLCCGAMS..........ARTAECPGPAQNASPLVLPP 382

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters:       2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       UniProt_05.80:*
                 1:  uniprot_sprot:*
                 2:  uniprot_trembl:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 2018 | 100.0 | 382 | 2 | Q6GRB6_HUMAN | Q6grb6 homo sapien |
| 2 | 2010 | 99.6 | 382 | 1 | FETUB_HUMAN | Q9ugm5 homo sapien |
| 3 | 2005 | 99.4 | 382 | 2 | Q6DK58_HUMAN | Q6dk58 homo sapien |
| 4 | 1783.5 | 88.4 | 345 | 2 | Q5J876_HUMAN | Q5j876 homo sapien |
| 5 | 1608.5 | 79.7 | 317 | 2 | Q5J875_HUMAN | Q5j875 homo sapien |
| 6 | 1318.5 | 65.3 | 387 | 2 | Q58D62_BOVIN | Q58d62 bos taurus |
| 7 | 1263 | 62.6 | 388 | 1 | FETUB_MOUSE | Q9qxc1 mus musculu |
| 8 | 1263 | 62.6 | 403 | 2 | Q6YJU2_MOUSE | Q6yju2 mus musculu |
| 9 | 1259 | 62.4 | 388 | 2 | Q8CB17_MOUSE | Q8cb17 mus musculu |
| 10 | 1207.5 | 59.8 | 378 | 1 | FETUB_RAT | Q9qx79 rattus norv |
| 11 | 1201.5 | 59.5 | 393 | 2 | Q6IRS6_RAT | Q6irs6 rattus norv |
| 12 | 1053.5 | 52.2 | 308 | 2 | Q6YJU1_MOUSE | Q6yju1 mus musculu |
| 13 | 466 | 23.1 | 392 | 2 | Q5HZU6_XENTR | Q5hzu6 xenopus tro |
| 14 | 453.5 | 22.5 | 412 | 2 | Q4LDQ0_XENTR | Q4ldq0 xenopus tro |
| 15 | 436 | 21.6 | 415 | 2 | Q6GLH1_XENTR | Q6glh1 xenopus tro |